Amendment to the Claims:

Please cancel claims 1 to 41 and 56 to 92, without prejudice.

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 41 (canceled)

Claim 42 (currently amended): A method of generating a nucleic acid encoding a carboxymethyl cellulase [[variant]] comprising:

(a) providing [[obtaining]] a nucleic acid comprising (i) a sequence encoding a carboxymethyl cellulase and having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1, ~~sequences substantially identical thereto, sequences complementary thereto, fragments~~ (ii) a sequence encoding a carboxymethyl cellulase and comprising at least 30 consecutive nucleotides of a sequence having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1 ~~thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NO: 1~~, (iii) a sequence encoding a carboxymethyl cellulase that hybridizes to a nucleic acid having a sequence as set forth in SEQ ID NO:1 under conditions comprising 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 n/ml sheared and denatured salmon sperm DNA, or, (iv) sequences complementary to (i), (ii) or (iii); [[and]]

(b) varying the sequence in (a) by modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence; and

(c) selecting a modified sequence that encodes a carboxymethyl cellulase, thereby generating a nucleic acid encoding a carboxymethyl cellulase.

Claim 43 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble

mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 43 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by error-prone PCR.

Claim 44 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by shuffling.

Claim 45 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by oligonucleotide-directed mutagenesis.

Claim 46 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by assembly PCR.

Claim 47 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by sexual PCR mutagenesis.

Claim 48 (currently amended): the method of claim 42, wherein the modifications, deletions or additions are introduced by *in vivo* mutagenesis.

Claim 49 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by cassette mutagenesis.

Claim 50 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by recursive ensemble mutagenesis.

Claim 51 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by exponential ensemble mutagenesis.

Claim 52 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by site-specific mutagenesis.

Claim 53 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by gene reassembly.

Claim 54 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by gene site saturated mutagenesis (GSSM™).

Claims 56 to 92 (canceled)

Claim 93 (new): The method of claim 42, wherein the nucleic acid has a sequence having at least 55% sequence identity.

Claim 94 (new): The method of claim 93, wherein the nucleic acid has a sequence having at least 60% sequence identity.

Claim 95 (new): The method of claim 94, wherein the nucleic acid has a sequence having at least 65% sequence identity.

Claim 96 (new): The method of claim 95, wherein the nucleic acid has a sequence having at least 70% sequence identity.

Claim 97 (new): The method of claim 96, wherein the nucleic acid has a sequence having at least 75% sequence identity.

Claim 98 (new): The method of claim 97, wherein the nucleic acid has a sequence having at least 80% sequence identity.

Claim 99 (new): The method of claim 98, wherein the nucleic acid has a sequence having at least 85% sequence identity.

Claim 100 (new): The method of claim 99, wherein the nucleic acid has a sequence having at least 90% sequence identity.

Claim 101 (new): The method of claim 100, wherein the nucleic acid has a sequence having at least 95% sequence identity.

Claim 102 (new): The method of claim 101, wherein the nucleic acid has a sequence having at least 97% sequence identity.

Claim 103 (new): The method of claim 102, wherein the nucleic acid has a sequence as set forth in SEQ ID NO:1.

Claim 104 (new): The method of claim 42, wherein the sequence of (ii) comprises at least 50 consecutive nucleotides.

Claim 105 (new): The method of claim 104, wherein the sequence comprises at least 75 consecutive nucleotides.

Claim 106 (new): The method of claim 105, wherein the sequence comprises at least 100 consecutive nucleotides.

Claim 107 (new): The method of claim 106, wherein the sequence comprises at least 150 consecutive nucleotides.

Claim 108 (new): The method of claim 107, wherein the sequence comprises at least 200 consecutive nucleotides.

Claim 109 (new): A method of generating a carboxymethyl cellulase comprising:

(a) providing a nucleic acid comprising (i) a sequence encoding a carboxymethyl cellulase and having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1, (ii) a sequence encoding a carboxymethyl cellulase and comprising at least 30 consecutive nucleotides of a sequence having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1, (iii) a sequence encoding a carboxymethyl cellulase that hybridizes to a nucleic acid having a sequence as set forth in SEQ ID NO:1 under conditions comprising 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 n/ml sheared and denatured salmon sperm DNA, or, (iv) sequences complementary to (i), (ii) or (iii);

(b) varying the sequence of (a) by modifying one or more nucleotides in the sequence to another nucleotide, deleting one or more nucleotides in the sequence, or adding one or more nucleotides to the sequence of (a); and

(c) selecting a modified sequence that encodes a carboxymethyl cellulase, thereby generating a nucleic acid encoding a carboxymethyl cellulase.

Claim 110 (new): A method of making a variant of a nucleic acid encoding a carboxymethyl cellulase comprising:

(a) providing a nucleic acid comprising (i) a sequence encoding a carboxymethyl cellulase and having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1, (ii) a sequence encoding a carboxymethyl cellulase and comprising at least 30 consecutive nucleotides of a sequence having at least 50% sequence identity to a nucleic acid as set forth in SEQ ID NO:1, (iii) a sequence encoding a carboxymethyl cellulase that hybridizes to a nucleic acid having a sequence as set forth in SEQ ID NO:1 under conditions comprising 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 n/ml sheared and denatured salmon sperm DNA, or, (iv) sequences complementary to (i), (ii) or (iii); and

(b) making a variant sequence of (a) by modifying one or more nucleotides in the sequence to another nucleotide, deleting one or more nucleotides in the sequence, or adding one or more nucleotides to the sequence of (a).